

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 24, 2002, 22:21:02 ; Search time 26 seconds  
(without alignments)  
660.431 Million cell updates/sec

Title: US-09-708-724a-2  
Perfect score: 2187  
Sequence: 1 MGPSVVVLCMKQLGQAL.....LLAVTREGLEIRISKRRAE 414

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	135.5	6.2	563	1 ARX_MOUSE	Q35085 mus musculu
2	131	6.0	2090	1 HFC1_MESAU	P51611 mesocricetu
3	121.5	5.6	1395	1 IF4G_HUMAN	Q04637 homo sapien
4	119	5.4	741	1 GTSE_MOUSE	Q8r080 mus musculu
5	117.5	5.4	1402	1 IF4G_RABIT	P41110 oryctolagus
6	116	5.3	3149	1 TEGU_EBV	P03186 epstein-bar
7	112.5	5.1	584	1 BCAS_HUMAN	O75363 homo sapien
8	112.5	5.1	1386	1 ZAP3_MOUSE	Q9r017 mus musculu
9	111.5	5.1	792	1 PCAP_MOUSE	Q924h2 mus musculu
10	111.5	5.1	2220	1 CAB1_HUMAN	O9y6j0 homo sapien
11	111	5.1	728	1 VIV_ORYSA	P37398 oryza sativ
12	110.5	5.1	1146	1 CCAS_RAT	Q02485 rattus norv
13	110.5	5.1	1290	1 PER1_HUMAN	O15534 homo sapien
14	110	5.0	817	1 VRP1_YEAST	P37370 saccharomyc
15	110	5.0	2142	1 BAT2_HUMAN	P48634 homo sapien
16	109.5	5.0	1575	1 SVJ1_HUMAN	O43426 homo sapien
17	109	5.0	883	1 PCGB_RAT	P55068 rattus norv
18	109	5.0	1004	1 SAL2_MOUSE	Q9q36 mus musculu
19	107.5	4.9	599	1 RF2P_DROSI	Q4629 drosophilla
20	107	4.9	1260	1 ALS1_CANAL	P46590 candida alb
21	107	4.9	1388	1 CAIE_HUMAN	P39059 homo sapien
22	106.5	4.9	365	1 VNSA_HPBDC	P30029 duck hepati
23	106	4.8	620	1 EXTN_TOBAC	P13983 nicotiana t
24	106	4.8	633	1 LA17_YEAST	Q12446 saccharomyc
25	106	4.8	838	1 TAC3_HUMAN	Q9y6as homo sapien
26	106	4.8	1233	1 NME3_HUMAN	Q14957 homo sapien
27	106	4.8	1822	1 ZAP3_HUMAN	P49750 homo sapien
28	105.5	4.8	626	1 GPBA_HUMAN	P07359 homo sapien
29	105.5	4.8	743	1 TLE2_HUMAN	Q04725 homo sapien
30	105.5	4.8	1210	1 TRX2_HUMAN	P51825 homo sapien
31	105.5	4.8	2715	1 AF4_HUMAN	Q9um66 homo sapien
32	105	4.8	671	1 CHS5_YEAST	Q12114 saccharomyc
33	105	4.8	751	1 TAU_RAT	P19332 rattus norv

RESULT 1				
ARX_MOUSE	ARX_MOUSE	STANDARD;	PRT;	563 AA.
ID	AC	O35085;		
DT	15-JUL-1999	(Rel. 38, Created)		
DT	15-JUL-1999	(Rel. 38, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	Homeobox protein ARX.			
GN	ARX.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97398450; PubMed=9256348;			
RA	Miura H., Yanazawa M., Kato K., Kitamura K.;			
RT	"Expression of a novel aristless related homeobox gene 'Arx' in the vertebrate telencephalon, diencephalon and floor plate.";			
RL	Mech. Dev. 65:99-109(1997).			
CC	-!- SUBCELLULAR LOCATION: Nuclear (By similarity).			
CC	-!- SIMILARITY: BELONGS TO THE PAIRED HOMEBOX FAMILY.			
CC	-!- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.			
CC	-!- SIMILARITY: CONTAINS 1 OAR DOMAIN.			
CC	-----			
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CC	-----			
DR	EMBL; AB006103; BAA28284.1; -.			
DR	HSSP; P06601; IFJL.			
DR	MGI; MGI:1097716; Arx.			
DR	InterPro; IPR000047; HTH_repressr.			
DR	InterPro; IPR003654; Homeo_OAR.			
DR	InterPro; IPR001356; Homeobox.			
DR	Pfam; PF00046; homeobox; 1.			
DR	PRINTS; PR00024; HOMEBOX.			
DR	PRINTS; PR00031; HTHREPRESSR.			
DR	PRODom; PD000010; Homeobox; 1.			
DR	SMART; SM00389; HOX; 1.			
DR	PROSITE; PS00027; HOMEBOX_1; 1.			
DR	PROSITE; PS50071; HOMEBOX_2; 1.			
DR	PROSITE; PS50803; OAR; 1.			
KW	Homeobox; DNA-binding; Nuclear protein.			
FT	DNA_BIND 330 389 HOMEBOX.			
FT	DOMAIN 531 544 OAR.			
FT	DOMAIN 100 116 POLY-ALA.			
FT	DOMAIN 127 132 POLY-PRO.			
FT	DOMAIN 143 154 POLY-ALA.			
FT	DOMAIN 183 186 POLY-PRO.			
FT	DOMAIN 231 241 POLY-GLU.			
FT	DOMAIN 274 285 POLY-ALA.			

P54258 rattus norv  
Q10172 schizosacch  
Q9y566 homo sapien  
Q03157 mus musculu  
O02193 drosophila  
P07261 saccharomyc  
P52212 candida alb  
P55200 mus musculu  
O14427 candida alb  
P25623 saccharomyc  
Q9wt13 rattus norv  
Q9qx47 mus musculu

ALIGNMENTS



QY 329 LREVEWPGRGH-----MAATCKKLV-----EGQRTMSLAAAPVREAPPPTG 372  
 Db 1572 LQASSTPLGSESSELSAQTPELQAAVDLSTGDPSSGQEPSSAVVATVVQPPPTQ 1631  
 QY 373 AS-SEPSVPALPGADPQPSAEILL-----LAVT 399  
 Db 1632 SEVDLSLPQELMAEAQAAGTTLMVGLTPELAVT 1667

RESULT 3  
 IF4G\_HUMAN  
 ID IF4G\_HUMAN STANDARD; PRT; 1395 AA.  
 AC Q04637;  
 AD 01-FEB-1995 (Rel. 31, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Eukaryotic translation initiation factor 4 gamma (eIF-4-gamma) (eIF-4G) (eIF4G) (P220).  
 DE 4G) (eIF4G) (P220).  
 GN EIF4G1 OR EIF4G.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=93054654; PubMed=1429670;  
 RA Yan R., Rychlik W., Etchison D., Rhoads R.E.;  
 RT "Amino acid sequence of the human protein synthesis initiation factor eIF-4 gamma.";  
 RL J. Biol. Chem. 267:23226-23231(1992).  
 RN [2]  
 RP SEQUENCE OF 408-525 FROM N.A.  
 RX MEDLINE=95379845; PubMed=7651417;  
 RA Mader S., Lee H., Pause A., Sonenberg N.;  
 RT "The translation initiation factor eIF-4E binds to a common motif shared by the translation factor eIF-4 gamma and the translational repressors 4E-binding proteins.";  
 RL Mol. Cell. Biol. 15:4990-4997(1995).  
 CC -!- FUNCTION: COMPONENT OF THE PROTEIN COMPLEX EIF-4, WHICH IS INVOLVED IN THE RECOGNITION OF THE MRNA CAP, ATP-DEPENDENT UNWINDING OF 5'-TERMINAL SECONDARY STRUCTURE AND RECRUITMENT OF MRNA TO THE RIBOSOME.  
 CC -!- PTM: PHOSPHORYLATED AT MULTIPLE SITES IN VIVO.  
 CC -!- SIMILARITY: THE C-TERMINAL REGION IS SIMILAR TO THE N-TERMINAL REGION OF WHEAT GERMINAL INITIATION FACTOR (ISO)4F SUBUNIT P82.  
 CC -----  
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 CC -----  
 DR EMBL; D12686; BAA02185.1; -;  
 DR Genbank; HGNC:3296; EIF4G1.  
 DR MIM; 600495; -;  
 DR InterPro; IPR003890; IF\_eIF4G.  
 DR InterPro; IPR003891; IF\_eIF4G\_MA3.  
 DR InterPro; IPR000504; RNA\_rec\_mot.  
 DR InterPro; IPR003307; eIF5C.  
 DR Pfam; PF02020; W2; 1.  
 DR Pfam; PF02847; MA3; 1.  
 DR Pfam; PF02854; MIF4G; 1.  
 DR SMART; SM00544; MA3; 1.  
 DR SMART; SM00543; MIF4G; 1.  
 DR SMART; SM00515; eIF5C; 1.  
 KW Initiation factor; Protein biosynthesis; Phosphorylation;  
 KW RNA-binding.  
 FT DOMAIN 258 271 POLY-GLU.  
 FT DOMAIN 305 308 POLY-ALA.  
 FT CONFLICT 497 500 PRGP -> ARGAQ (IN REF. 1).

SQ SEQUENCE 1395 AA; 153360 MW; C712A09D270DF2A8 CRC64;  
 Query Match 5.6%; Score 121.5; DB 1; Length 1395;  
 Best Local Similarity 24.1%; Pred. No. 1.4;  
 Matches 60; Conservative 28; Mismatches 92; Indels 69; Gaps 11;

QY 167 NKGGRSCONPALPQDQSPSQGNATTSTVTRDNYHLLTTEEEFGVWSQSMKWHSONKSGGVP 226  
 Db 40 SQGAIADRPGLGPEHSPS-----ESQSPSPSPPT 70

QY 227 VRGPTQEPCESEQLIKESFVPPT-----TPKENNKQRE-DENWRLPPPPVAETPPVSP 279  
 Db 71 SPSPVLEPGSEPNLAVLSIPGDTMTIOMSVSEETPSRETGETPYRLSPSP---TPLAEP 127

QY 280 SVTEIETPLQIPRTATITAGEPLGCHCTTISPAFVHSLNKRKRLLELLREVEWPGRGH 339  
 Db 128 -LLEVEVTLSPVSESEFSSPLQAPT-----PLASHTV-----EIHEP-NGM 168

QY 340 MAATCKKLVQEGQDRTMSLAAAPVREAPP--PT-----GASSEPSVPALPGADPQR 389  
 Db 169 VPSEDLPEVESSPELAPPACP-SESPVPIAPTAQPELLNGAPSPPAVDLSVPSEDEE 227

QY 390 SAEILLIAY 398  
 Db 228 QAKEVTASV 236

RESULT 4  
 GTSE\_MOUSE  
 ID GTSE\_MOUSE STANDARD; PRT; 741 AA.  
 AC Q8R080; Q89015; Q9CGS9;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE G2 and S phase expressed protein 1 (gtse-1) (B99 protein).  
 GN GTSE1 OR B99.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98393542; PubMed=9724637;  
 RA Utrera R., Collavin L., Lazarevic D., Delia D., Schneider C.;  
 RT "A novel p53-inducible gene coding for a microtubule-localized protein with G2-phase-specific expression.";  
 RL EMO J. 17:5015-5025(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Strausberg R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 1-130 FROM N.A.  
 RX STRAIN=C57BL/6J; TISSUE=Embryo;  
 RC MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,  
 RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nombarts P.,  
 RA Nordone P., King B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [4]  
RX PubMed:10984615;  
RA Collavin L., Monte M., Verardo R., Pflieger C., Schneider C.;  
RT "Cell-cycle regulation of the p53-inducible gene B99.";  
RL FEBS Lett. 481:57-62(2000).  
CC -!- FUNCTION: May be involved in p53-induced cell cycle arrest in G2/M  
CC phase by interfering with microtubule rearrangements that are  
CC required to enter mitosis. Overexpression delays G2/M phase  
CC progression.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Associated with microtubules.  
CC -!- DEVELOPMENTAL STAGE: Expression begins at S phase, accumulates in  
CC late S/G2 phase and disappears in G1 phase.  
CC -!- PTM: Phosphorylated in mitosis.  
CC -!- INDUCTION: By p53 when exposed to different DNA damaging  
CC agents, including gamma irradiation and chemotherapeutic drugs.  
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CC  
CC EMBL; AJ222580; CAA10848.1; -  
DR EMBL; BC027213; AAH27213.1; -  
DR EMBL; AK012870; BAB28524.1; -  
DR MGD; MGI:1352755; Gtse1.  
KW Microtubules; Phosphorylation.  
FT DOMAIN 23 28  
FT POLY-SER.  
FT CONFLICT 153 153 S -> P (IN REF. 2).  
FT CONFLICT 246 246 I -> L (IN REF. 2).  
FT CONFLICT 252 252 V -> M (IN REF. 2).  
FT CONFLICT 274 274 S -> G (IN REF. 2).  
FT CONFLICT 398 399 SP -> IL (IN REF. 2).  
FT CONFLICT 741 741 AA; 78751 MW; 1C684D06E9B7ACB CRC64;  
SQ SEQUENCE 741 AA; 78751 MW; 1C684D06E9B7ACB CRC64;  
  
Query Match  
Best Local Similarity 5.4%; Score 119; DB 1; Length 741;  
Matches 109; Conservative 47; Mismatches 174; Indels 184; Gaps 24;  
  
QY 32 NOGKRCPCFGAQLMTCQNTPLPSVSHRS-PPGNA-----AVSVTGDCDL 76  
DB 185 NOG-----LPCSSQPLPRESSTQSPSQAGPQKRITKSLQPPRALPVRGNLHL 233  
QY 77 PTE---EFGVLVQSMKCDTVRIK---VLOG-PTTAPPLMTSE----- 113  
DB 234 ATEKLKKEVPASTQRTK--LVNEKGSQSDVLQDKPSTADPAASREGHPCKRSILPIPGKLG 291  
QY 114 -----GNVTAED-----TEAIRAFVYAAASAAEAWHRHVLVLSGGQIHPEI 157  
DB 292 LAKTLTKPPGYTGNLTTRKSTSGSASSLESYGVRSSVAGKAKSSSEORSSIPASGSORR--- 349  
QY 158 GSGGNIINTNKGR---SCQNALPS----- 180  
DB 350 -----TSTSKSGRIGPAASRQALPAARVFGQANKADAAQTVAEQKVPFTLSPLTQ 403  
QY 181 -----PD-QSPSGNATTSV-TRDNYHLLTEEEFGVMSQSMK---WHSQNKSGG 223  
DB 404 PQTPEQGRPLPDDETPTPOLNTKVTSLKRDSDVLSCKTEAVSTTTPFKVPQFSVGESPGG 463  
QY 224 SVVVRGPTQPCSESOILKESFVPTTPKENNKQEREDENWRLPPPPVAETVPVPSVYTE 283  
DB 464 VTPKFSRTHR-----LQSWTPASRVVSSSTPVRRSSGCTTQGLPGSMRTPLSTRMSV 515  
QY 284 IETPLOR-----IPRTATIGEPLGCHCTFTTISPAFV-----HVLNKRKKQLLELLREVEN 334  
DB 516 LPTPASRRLLSLPLMA-----PQSMPRALVSLPLCPARLKSSEPRRRSTVRAELTQESSG 570

QY 335 PGRGHMAATCKCKLQVEGQDRMTS-----LAAAPVREAPPPTGTAS-----SEPSV 379  
DB 571 SGGGQA-----QGLSSDESSPPSSVPQALNFSPEKSASPPQGSSTGAAGAEAPPE 624  
QY 380 PALP-----GADPORSRELLL-----LAVTRE 401  
DB 625 DTLPLSEVHGCGSHTPSEGLLDLKLQTLTIPPE 658  
RESULT 5  
EIF4G\_RABIT STANDARD; PRT; 1402 AA.  
AC IF4G\_RABIT  
AC P41110;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Eukaryotic translation initiation factor 4 gamma (eIF-4-gamma) (eIF-4G) (eIF4G) (p220).  
DE 4G) (eIF4G) (p220).  
GN EIF4G.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 479-500.  
RC STRAIN-New Zealand white; TISSUE-Brain;  
RX MEDLINE=93374895; PubMed=8396129;  
RA Lauphear B.J., Van R., Yang F., Waters D., Liebig H.-D.,  
RA Klump H., Kuechler E., Skern T., Rhoads R.E.;  
RT "Mapping the cleavage site in protein synthesis initiation factor  
RT eIF-4 gamma of the 2A proteases from human Cocksackievirus and  
RT rhinovirus.";  
RL J. Biol. Chem. 268:19200-19203(1993).  
RN [2]  
RP PARTIAL SEQUENCE.  
RX MEDLINE=93054654; PubMed=1429670;  
RA Yan R., Rychlik W., Etchison D., Rhoads R.E.;  
RT "Amino acid sequence of the human protein synthesis initiation factor  
RT eIF-4 gamma.";  
RL J. Biol. Chem. 267:23226-23231(1992).  
CC -!- FUNCTION: COMPONENT OF THE PROTEIN COMPLEX EIF-4, WHICH IS  
CC INVOLVED IN THE RECOGNITION OF THE MRNA CAP, ATP-DEPENDENT  
CC UNWINDING OF 5'-TERMINAL SECONDARY STRUCTURE AND RECRUITMENT OF  
CC MRNA TO THE RIBOSOME.  
CC -!- SIMILARITY: THE C-TERMINAL REGION IS SIMILAR TO THE N-TERMINAL  
CC REGION OF WHEAT EUKARYOTIC INITIATION FACTOR (ISO)4F SUBUNIT P82.  
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CC  
CC EMBL; L22090; AAA31242.1; -  
DR InterPro; IPR003890; IF\_eIF4G.  
DR InterPro; IPR003891; IF\_eIF4G\_MA3.  
DR InterPro; IPR000504; RNA\_rec\_mot.  
DR InterPro; IPR003307; eIF5C.  
DR Pfam; PF02020; W2; 1.  
DR Pfam; PF02847; MA3; 1.  
DR Pfam; PF02854; MIF4G; 1.  
DR SMART; SM00544; MA3; 1.  
DR SMART; SM00543; MIF4G; 1.  
DR SMART; SM00515; eIF5C; 1.  
KW Initiation factor; Protein biosynthesis; Phosphorylation;  
KW RNA-binding.  
FT DOMAIN 188 192 POLY-PRO.  
FT DOMAIN 262 275 POLY-GLU.  
FT DOMAIN 1393 1398 POLY-GLU.  
SQ SEQUENCE 1402 AA; 154050 MW; 7FD85D7E30519230 CRC64;





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FT DOMAIN 180 199 POLY-GLN.
FT DOMAIN 211 222 POLY-GLN.
FT DOMAIN 230 242 POLY-GLN.
FT DOMAIN 246 259 POLY-GLN.
FT DOMAIN 453 460 POLY-PRO.
FT DOMAIN 603 609 POLY-PRO.
SQ SEQUENCE 792 AA; 87061 MW; 71C879DCD3925E62 CRC64;

Query Match 5.1%; Score 111.5; DB 1; Length 792;
Best Local Similarity 22.8%; Pred. No. 3.4;
Matches 87; Conservative 49; Mismatches 145; Indels 101; Gaps 20;

Oy 33 QGKRCPCGCAQLMTCNQPTLPVSHRSPGNAAVSVTGDCGCHLPTEEFGLVQSMKCD 92
Db 301 QAOQSPI--AQN---QPPQIPQSQSQPLVSRQAQALPGPMLYAAQQO-----LK 344
Oy 93 TVRIKGVLOGTTPAPLMTSGNVTAEDETEAIRAFVYAVAAASAAEAWHRLVLLSG- 151
Db 345 FVRAPMVVQOVQOVQOVQOVQOVQ-----AAVQAQSAQ-----MVAPGV 387
Oy 152 -QIHEPIGSGNIINTNKGGRSCONPALPSPDQSPGNATTSVTRDNYHLLTEEEFG-- 207
Db 388 QMIAEALAQGHVRAFPPTSTWS-AGPSSSISLGGQPTTVQSGSSUTMLSSPSPGQOV 446
Oy 208 VWSQSMKWHSO-NKSGGSPV---VRGPTQPCSESQILKESFVPPPTPKENNK--QERE 260
Db 447 QTPQSMPPPPQSPQSPQSPNSVSSGPAASP-----SSFLPSPSPQSPQSVTART 498
Oy 261 DENWRLPPPPVAETPVPSPV-----TEIETPLQRIPTATYATAGPLGHCFTTISPA 312
Db 499 PNFVSVPSPGLPNTVPNPSVMSFAGSSQAEEQQYLDKQLSKYI-BPL----- 547
Oy 313 FVHSLVNLK-----RKROL-----ELLREVWPGRGHMAATC--CKLOVEGDQRTMSLAA 361
Db 548 --RMINKIDNEDKKDLKSKLSLLDITDPSKRCPLTKQCEIALEKLNDAV--- 602

Oy 362 PVREAPPPPTGASPSVPALP 383
Db 603 ---PTPPPP-----PVLP 612

RESULT 10
CABI_HUMAN STANDARD: PRT: 2220 AA.
AC Q9Y6J0; Q9Y460;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcineurin-binding protein Cabin 1 (Calcineurin inhibitor) (CAIN).
GN CABIN1 OR KIA00330.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=98318216; PubMed=9655484;
RA Sun L., Yoon H.-D., Loh C., Stelow M., He W., Liu J.O.;
RT "Cabin 1, a negative regulator for calcineurin signaling in T
RL lymphocytes.";
RN Immunity 8:703-711(1998).

[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
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RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Grahame D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L., Swann R.M.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Mala J.E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,
RA Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,
RA McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyraud M., Kedra D.,
RA Serousi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
RA Wilkison P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
RA Tilahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).

[3]
RN SEQUENCE OF 319-2220 FROM N.A.
RP TISSUE=Brain;
RX MEDLINE=97349984; PubMed=9205841;
RA Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. VII.
RL The complete sequences of 100 new cDNA clones from brain which can
CC code for large proteins in vitro.";
CC DNA Res. 4:141-150(1997).
CC -!- FUNCTION: IT MAY SERVE AS A NEGATIVE REGULATOR OF T CELL RECEPTOR
CC (TCR) SIGNALING VIA INHIBITION OF CALCINEURIN. INTERACTS WITH AND
CC INHIBITS CALCINEURIN-MEDIATED SIGNAL TRANSDUCTION. CABIN 1 IS
CC SPECIFIC FOR THE ACTIVATED FORM OF CALCINEURIN, THEIR INTERACTION
CC IS DEPENDENT ON BOTH PKC AND CALCIUM SIGNALS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN DIFFERENT TISSUES.
CC -!- PTM: ACTIVATED THROUGH PKC-MEDIATED HYPERPHOSPHORYLATION.
CC -!- SIMILARITY: CONTAINS 6 TPR REPEATS.
CC -----
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CC -----
CC EMBL; AF072441; AAD40846.1; -
CC EMBL; AP000352; -; NOT_ANNOTATED_CDS.
CC EMBL; AP000353; -; NOT_ANNOTATED_CDS.
CC EMBL; Z92546; CAB62954.1; -
CC EMBL; AB002328; BAA20788.1; -
CC MIM; 604251; -
CC InterPro; IPR001440; TPR.
CC Pfam; PF00515; TPR; 4.
CC SMART; SM00028; TPR; 3.
CC phosphorylation; Repeat; TPR repeat.
KW
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FT REPEAT 36 69 TPR 1.
FT REPEAT 90 123 TPR 2.
FT REPEAT 125 157 TPR 3.
FT REPEAT 615 648 TPR 4.
FT REPEAT 1055 1088 TPR 5.
FT REPEAT 1106 1139 TPR 6.
FT DOMAIN 2116 2153 CALCINEURIN BINDING (BY SIMILARITY).
SQ SEQUENCE 2220 AA; 246350 MW; BA4AD1741056C233 CRC64;

Query Match
Best Local Similarity 5.1%; Score 111.5; DB 1; Length 2220;
Matches 104; Conservative 39; Mismatches 171; Indels 147; Gaps 21;

QY 10 VCGMKOLGALQASVLSIITENQGRKPCFGAQNLMTCQNTPLPSVSHRSPGNAAVSV 69
DB 1678 VCGLP--GARMTTDVS-----HKASPEDQOGL---PQPKPLADSGPGPEPGK 1724
QY 70 TGGDCHLPTFEFEGVLVQSMKCDTVRIKVLQ-----GPTTAPPLMTSEGNVTAEDTE 122
DB 1725 VGLLNHRPVAMDAG-----DSADQSGERKDKESPRAGPT--EPMDDTSEATVCHSDLE 1774
QY 123 EAIRAFVVAARASAAEA---WHNRHLVLLSQIHEPIGSGNININTKGRSQNPAL 178
DB 1775 RTPPLLPGRAPDRGPESRPTLSLELSISARQOQPTPL-----TPAQ 1817
QY 179 PSPDQSPSGNATTSVTRONYH-----LITEEEFG-----VWSQSMKWH 216
DB 1818 PAPAPAP---ATTGTRAGGHEEPLSLRSRKRKLLLEDTESKTLLLDAYRVWQOGOK-- 1872
QY 217 SONKGGSVVPGVPGQPCSESOIL-----KESFVPPPT 249
DB 1873 -----GVAYDLGRVERIMSETYMLIKQVDEEALEQAVKFCQVHLGAAQRAQSGDTP 1926
QY 250 TPKENNKQEREDENRLPPPPVAETVPSPSVTELETPLQRTIATRTIATGEPLGHTCTFI 309
DB 1927 TPK--HPKDSREN--FPVTVVTPADVPADSV--QRPDAHTKPRALAAATTI-----ITC 1979
QY 310 SPAFVHSLNKKRQLELLLEVEWPG-----RGHMAATCCCKLOVEGQD--RTMSLAAP 362
DB 1980 PFSASASTLDQSKD-----PGPPRPHRPEATPSMISGLPEGEELARVAEGTSFP 2028
QY 363 VREAPPPPTGASSEFSPVLPAL-----GADPQRSAAE 392
DB 2029 PQEPRHSQVQKMAPTSSPAEPHCWFAEALGTGAETCSQE 2069

RESULT 11
VIV_ORYSA STANDARD; PRT: 728 AA.
AC P37398;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Viviparous protein homolog.
GN VPI.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94250843; PubMed=8193305;
RA Hattori T., Terada T., Hamauna S.;
RT "Sequence and functional analyses of the rice gene homologous to the
maize Vpi.";
RL Plant Mol. Biol. 24:805-810(1994).
CC -!- FUNCTION: COULD PARTICIPATE IN ABSICISIC ACID-REGULATED GENE
EXPRESSION DURING SEED DEVELOPMENT.
CC -!- SIMILARITY: CONTAINS 1 TF-B3 DOMAIN.
CC -----
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CC -----
DR EMBL; D16640; BAA04066.1; -.
DR PIR; S48899; S48899.
DR TRANSFAC; T04785; -.
DR InterPro; IPR003340; TF_B3.
DR Pfam; PF02362; B3; 1.
KW Developmental protein; Transcription regulation; DNA-binding;
KW Activator.
FT DOMAIN 500 685 TF-B3.
SQ SEQUENCE 728 AA; 75982 MW; F66882079F5FE428 CRC64;

Query Match
Best Local Similarity 5.1%; Score 111; DB 1; Length 728;
Matches 67; Conservative 29; Mismatches 114; Indels 92; Gaps 15;

QY 170 GRSCONPALPSD-----QSPSGN-----ATTSVTRONYHLLTEEFVGSQSMKWHSQ 218
DB 257 GAASDQPLSPCANPGVEFFSGQEMGSAATS-----WMPYQAFTPP 300
QY 219 NKSGSVVRG-----PTQPCSESOILKES--FVPTTPKENNKQEREDENRLP----- 267
DB 301 AAYGDAMPYGAAGPPEPQQSCSKSVVVSQFPPTAAAAGDMHASGGGNWAPQOFA 360
QY 268 PPVVAETVPSPSVTEIETPLQRTIATRTIATGE-PLGHTCTF-----ISPAFVHSLNKK- 320
DB 361 PFPVST--SSYTMPSPVPP-----PFTAGFPGQYSGGHAMCSPRLAGVPESTKEARKR 414
QY 321 --RKQLELLLEVEWPGRGHMAATCCCKLOVEGQDRTMSLAAA----- 361
DB 415 MARQRLSCLOQ-----RSQQLNSQIHSHGHQEPSRAHSAVPYTPSSAGCSWGI 468
QY 362 -----PVREAPPPPTGASSEFS--VPALPGADPQPSAELLALLAVTREGLEIRISR 410
DB 469 WPPAAQIIQNPLSNPNPPATSKQPKSPKPKPQAAA-----TAGAESLQSTASE 523
QY 411 KR 412
DB 524 KR 525

RESULT 12
CCAS_RAT STANDARD; PRT: 1146 AA.
AC Q02485; Q01553; P70484; Q62817;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Voltage-dependent L-type calcium channel alpha-1S subunit (Calcium
channel, L type, alpha-1 polypeptide, isoform 3, skeletal muscle)
DE (ROB1) (Fragment).
GN CACNA1S OR CACNA1 OR CACN1 OR CCHLIA3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93122775; PubMed=1335956;
RA Chin H., Krall M., Kim H.-L., Kozak C.A., Mock B.A.;
RT "The gene for the alpha-1 subunit of the skeletal muscle
RT dihydropyridine-sensitive calcium channel (Cchla3) maps to mouse
chromosome 1.";
RL Genomics 14:1089-1091(1992).
RN [2]
RP SEQUENCE OF 597-691 FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93066265; PubMed=1279681;
RA Yu A.S.L., Hebert S.C., Brenner B.M., Lytton J.;
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"Molecular characterization and nephron distribution of a family of transcripts encoding the pore-forming subunit of Ca<sup>2+</sup> channels in the kidney.";  
Proc. Natl. Acad. Sci. U.S.A. 89:10494-10498(1992).  
[3]  
SEQUENCE OF 359-658 FROM N.A. (ISOFORM ROB1).  
TISSUE-Osteosarcoma;  
MEDLINE=96074617; PubMed=7479909;  
RA Barry E.L.R., Gesek F.A., Froehner S.C., Friedman P.A.;  
RT "Multiple calcium channel transcripts in rat osteosarcoma cells:  
selective activation of alpha 1D isoform by parathyroid hormone.";  
Proc. Natl. Acad. Sci. U.S.A. 92:10914-10918(1995).  
[4]

PHOSPHORYLATION BY CAPK.  
MEDLINE=91065881; PubMed=2174428;  
RA Lai Y., Seagar M.J., Takahashi M., Catterall W.A.;  
RT "Cyclic AMP-dependent phosphorylation of two size forms of alpha 1  
subunits of L-type calcium channels in rat skeletal muscle cells.";  
J. Biol. Chem. 265:20839-20848(1990).  
CC -!- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE  
ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED  
IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE  
CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,  
CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1S  
GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE)  
CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA)  
GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP).  
CC PHENYLALANINES, BENZOTHAZEPINES, AND BY OMEGA-AGATOXIN-LIITA  
(OMEGA-AGA-LIITA). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-  
GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).  
CC CALCIUM CHANNELS CONTAINING THE ALPHA-1S SUBUNIT PLAY AN IMPORTANT  
ROLE IN EXCITATION-CONTRACTION COUPLING IN SKELETAL MUSCLE.  
CC -!- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT  
COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS  
IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-  
FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS  
SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM  
CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA  
LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY. AN  
ADDITIONAL GAMMA SUBUNIT IS PRESENT ONLY IN SKELETAL MUSCLE L-TYPE  
CHANNEL.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: SKELETAL MUSCLE SPECIFIC.  
CC -!- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE  
HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE  
POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS  
PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A  
SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.  
CC -!- DOMAIN: THE LOOP BETWEEN REPEATS II AND III INTERACTS WITH THE  
RYANODINE RECEPTOR, AND IS THEREFORE IMPORTANT FOR CALCIUM RELEASE  
FROM THE ENDOPLASMIC RETICULUM NECESSARY FOR MUSCLE CONTRACTION.  
CC -!- PTM: PHOSPHORYLATION BY CAPK STIMULATES THE CALCIUM CHANNEL  
FUNCTION (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS  
FAMILY.  
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EMBL; L04684; AAA00844.1; -;  
DR EMBL; M99220; AAA40894.1; -;  
DR EMBL; U31816; AAA89158.1; -;  
DR InterPro; IPR001682; Ca/Na\_pore.  
DR InterPro; IPR002111; Cat\_channel\_Trlp.  
DR InterPro; IPR000636; M-channel\_nlg.  
DR Pfam; PF00520; Ion\_trans; 2.  
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
Calcium channel; Glycoprotein; Repeat; Multigene family;

KW	Calcium-binding; Phosphorylation; Alternative splicing.	1	
FT	NON-TER	1	III.
FT	REPEAT	73	IV.
FT	REPEAT	392	671
FT	DOMAIN	<1	86
FT	TRANSMEM	87	105
FT	DOMAIN	106	121
FT	TRANSMEM	122	141
FT	DOMAIN	142	153
FT	TRANSMEM	154	172
FT	DOMAIN	173	179
FT	TRANSMEM	180	198
FT	DOMAIN	199	217
FT	TRANSMEM	218	237
FT	DOMAIN	238	327
FT	TRANSMEM	328	352
FT	DOMAIN	353	405
FT	TRANSMEM	406	424
FT	DOMAIN	425	439
FT	TRANSMEM	440	459
FT	DOMAIN	460	467
FT	TRANSMEM	468	486
FT	DOMAIN	487	518
FT	TRANSMEM	519	537
FT	DOMAIN	538	556
FT	TRANSMEM	557	576
FT	DOMAIN	577	643
FT	TRANSMEM	644	668
FT	DOMAIN	669	1146
FT	SITE	301	301
FT	SITE	610	610
FT	BINDING	275	364
FT	BINDING	624	690
FT	BINDING	636	679
FT	MOD_RES	679	679
FT	CA_BIND	697	708
FT	CARBOHYD	428	428
FT	VARSPPLIC	491	509
FT	CONFLICT	548	548
FT	CONFLICT	610	610
FT	SEQUENCE	1146 AA;	130143 MW; 4BBE944261BE1A95 CRC64;
Qy	Query Match	5.1%;	Score 110.5; DB 1; Length 1146;
Qy	Best Local Similarity	22.8%;	Pred No. 6.1;
Qy	Matches	82;	Conservative 45; Mismatches 139; Indels 93; Gaps 17;
Qy	79	EEFGLVQSMKCDTVRIKGVQ--GPTTAPPLMTS-EGNVTAEDETEEAIRAFVAVAAA	135
Db	828	EEYGG---YRPKKTQVQIAGLRTIEEAAPEIHRASIGDLTAE--EELERAMVEA----	878
Qy	136	SAEAHHRHLVLLSGQIHEPIGSGGNININTKGRSC-----QN 175	
Db	879	AMEEGIFRTGGLFGVDNLFERTNSLPVMANORLQFAEMEMELESFVLEDFPON	937
Qy	176	PALPSPDQSPSNATSTVTRDNYHLLTEEEFGVWSQSMKWSQ--NKSGGSPVVRGPTQE	233
Db	938	PGTHPLARNTNANNAVYGNSSHRNSPVF---SSIKYRELLEEAAGRPTVRGPTSQ	993
Qy	234	PCSESQILKESFVPTTPKNNKQREDENWRLPPPPVAETPVP-----277	
Db	994	PCSVSGVNSRSHV-----DKLEROMSORMPKGPVPPSPCOLSOEKHPVHEBKGPR	1045
Qy	278	--SPSVTEIETPLQRIPTATTAGEPLGH-----CTFTISPAFVHSVINKRRKQLELL	329
Db	1046	SWSTETSDSESPERVPRNS-----AHKCTAPATTMLIQEALVRGGLDLSAADANFVM	1098
Qy	330	REVENPGRGHMAATCCKLQVEQDRTMSLAAAPV--REAPP--PPTCASSEPSVPALPGA	385
Db	1099	-----ATQALADACOMEPE-----EVEVAATELLKRPKGGPCGSLPKV--LPWA	1145

RESULT 13  
 PERI\_HUMAN STANDARD; PRT; 1290 AA.  
 AC O15534;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DE 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Period circadian protein 1 (Circadian pacemaker protein Rigiui) (hPER).  
 GN PERI OR PER OR RIGUI.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE=Heart;  
 RX MEDLINE=97462301; PubMed=9323128;  
 RA Sun Z.S., Albrecht U., Zhuchenko O., Bailey J., Eichele G., Lee C.C.;  
 RT "Rigiui, a putative mammalian ortholog of the Drosophila period gene.";  
 RL Cell 90:1003-1011(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=97472418; PubMed=9333243;  
 RA Tei H., Okamura H., Shigeyoshi Y., Fukuhara C., Ozawa R., Hirose M.,  
 RA Sakaki Y.;  
 RT "Circadian oscillation of a mammalian homologue of the Drosophila  
 RT period gene.";  
 RL Nature 389:512-516(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Hida A., Sakaki Y., Tei H.;  
 RX PubMed=10940553;  
 RT "Genomic structures of the human and mouse period1 genes.";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX PubMed=10940553;  
 RA Taruscio D., Zorraqi G.K., Falchi M., Iosi F., Paradisi S.,  
 RA Di Fiore B., Lavia P., Falbo V.;  
 RT "The human Perl gene: genomic organization and promoter analysis of  
 RT the first human orthologue of the Drosophila period gene.";  
 RL Gene 253:161-170(2000).  
 CC -!- FUNCTION: CIRCADIAN REGULATOR THAT MAY ACT AS A TRANSCRIPTION  
 CC FACTOR. BEHAVES AS A NEGATIVE ELEMENT IN CIRCADIAN TRANSCRIPTIONAL  
 CC LOOP. DOES NOT APPEAR TO BIND DNA, SUGGESTING INDIRECT  
 CC TRANSCRIPTIONAL INHIBITION. SEEMS TO BE THE PACEMAKER COMPONENT  
 CC WHICH RESPONDS TO LIGHT AND MEDIATES PHOTIC ENTRAINMENT. IN THE  
 CC SUPRACHIASMATIC NUCLEUS (SCN), IT BEHAVES LIKE A DAY-TYPE  
 CC OSCILLATOR, WITH MAXIMUM EXPRESSION DURING THE LIGHT PERIOD.  
 CC OSCILLATIONS ARE MAINTAINED UNDER CONSTANT DARKNESS AND ARE  
 CC RESPONSIVE TO CHANGES OF THE LIGHT/DARK CYCLES. THERE IS A 4 HOUR  
 CC TIME DELAY BETWEEN PER1 AND PER2 OSCILLATIONS. THE EXPRESSION  
 CC RHYTHMS APPEAR TO ORIGINATE FROM RETINA (BY SIMILARITY).  
 CC -!- SUBUNIT: FORMS A HETERODIMER, PROBABLY WITH CLOCK.  
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).  
 CC -!- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; RIGUI 4.7 (SHOWN HERE),  
 CC RIGUI 3.0 AND RIGUI 6.6/TRUNCATED; ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED. FOUND IN HEART, BRAIN,  
 CC PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, PANCREAS, AND AT LOW LEVEL  
 CC IN THE KIDNEY.  
 CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF  
 CC TRANSCRIPTION FACTORS.  
 CC -!- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.  
 CC -!- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.  
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 CC EMBL; AF022991; AAC51765.1; -  
 DR EMBL; AB002107; BAA22633.1; -  
 DR EMBL; AB030817; BAA94085.1; -  
 DR EMBL; AF102137; AAF15544.1; -  
 DR Genew; HGNC:8845; PER1.  
 DR MIM; 602260; -  
 DR InterPro; IPR001610; PAS.  
 DR InterPro; IPR000014; PAS\_domain.  
 DR Pfam; PF00989; PAS; 1.  
 DR SMART; SM00086; PAS; 1.  
 DR SMART; SM00091; PAS; 2.  
 DR PROSITE; PS01112; PAS; 1.  
 KW Transcription regulation; Nuclear protein; Repeat; Biological rhythms;  
 KW Alternative splicing.  
 FT DOMAIN 136 172 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).  
 FT DOMAIN 209 275 PAS 1.  
 FT DOMAIN 346 416 PAS 2.  
 FT DOMAIN 425 465 PAC.  
 FT DOMAIN 66 79 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT DOMAIN 69 75 POLY-SER.  
 FT DOMAIN 653 656 POLY-SER.  
 FT DOMAIN 1010 1013 POLY-PRO.  
 FT DOMAIN 1269 1273 POLY-GLU.  
 FT DOMAIN 1276 1279 POLY-SER.  
 SQ SEQUENCE 1290 AA; 136237 MW; 24B53042869A4562 CRC64;  
 Query Match 5.1%; Score 110.5; DB 1; Length 1290;  
 Best Local Similarity 20.1%; Pred. No. 7;  
 Matches 91; Conservative 42; Mismatches 162; Indels 157; Gaps 20;  
 QY 36 RCPFCGA--QNLMTQNTPLPSVSHRSPGNAASVTGGD----- 73  
 DB 576 RLPAATGTFKAKALPCQSPD-PELEAGSAPVQAPLALVPEEAERKEASSCYQINCLDSI 634  
 QY 74 -----CHLPTEEFGLVQSMKC-----DTVRKIGVLQGTPTAPPLMTSE 113  
 DB 635 LRYLESCNLP-----TTKRKACSSSYTTSSASDDDRQRTGPVSVGTKKDPSPSAALS 687  
 QY 114 GNVTAEDTEAFRAFYVAASAAENWHRLVLLSQ-----IHEPICS-----GCN 162  
 DB 688 GEGATPRKEPVVGGTLSPALANKAES-----VVSVTSQCSFSSSTIVH--VGDKKRPESD 740  
 QY 163 IINTNKGGRSCNPA---LPS-----PDQSPGNATTSVTRDNYHLTEEE----- 205  
 DB 741 IIMMEDLPLAGPAPSPAPSPVAPDPADPAPVGLTKAVLSLHTQEQEQAFLSRFRD 800  
 QY 206 -----FGVWSQSMKWHSONKSGGSPVVRGPTQE-PCSESQIL 241  
 DB 801 LGLRLGLDSSSTAPSGALGERGCHGFPAPPSRRHHCKSKAKSRHHQNPRAEAPCYVSH-- 858  
 QY 242 KESFVPPPTPKENNKOEDENNRLPPP---PVAETPVPSVTEIETPLQRIPTATI 297  
 DB 859 -PSPVPPSTP-----WPTTPATPPAVVQVPLPVFS-----PRGGP- 895  
 QY 298 AGEPLGHCTFTTISPAFVSHVNLKRRQLELLREVEWPGRHMAATCKLQVEGQDRTMS 357  
 DB 896 --QPLPAPPTSPVPAFAFPAPL--VTPMVALVLPNLYLFTPTSSYPYQALQTPAEG----- 945  
 QY 358 LAAAPVREAPPPTGASPSPSVDPALGPQQR 389  
 DB 946 -----PPTPASHSPSPSLPALPPSPPHR 968  
 RESULT 14  
 VRPL\_YEAST STANDARD; PRT; 817 AA.  
 ID VRPL\_YEAST  
 AC P37370; Q06133;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Verprolin.



KW	Repeat.	519	524	POLY-PRO.
FT	DOMAIN	636	657	GLN-RICH.
FT	DOMAIN	688		POLY-PRO.
FT	DOMAIN	699	704	POLY-PRO.
FT	DOMAIN	814	821	POLY-PRO.
FT	DOMAIN	1340	1345	POLY-GLY.
FT	DOMAIN	1398	1403	POLY-GLY.
FT	DOMAIN	1436	1442	POLY-PRO.
FT	DOMAIN	1982	1991	POLY-PRO.
FT	DOMAIN	41	1795	4 X 57 AA TYPE A REPEATS.
FT	REPEAT	41	95	1-1.
FT	REPEAT	98	154	1-2.
FT	REPEAT	281	337	1-3.
FT	REPEAT	1740	1795	1-4.
FT	DOMAIN	337	549	2 X TYPE B REPEATS.
FT	REPEAT	337	418	2-1.
FT	REPEAT	476	549	2-2.
FT	DOMAIN	1899	2089	3 X 50 AA TYPE C REPEATS.
FT	REPEAT	1899	1948	3-1.
FT	REPEAT	1965	2014	3-2.
FT	REPEAT	2040	2089	3-3.
FT	CONFLICT	57	57	R -> A (IN REF. 2).
FT	CONFLICT	109	109	Q -> S (IN REF. 2).
FT	CONFLICT	414	414	P -> PPHRGAGNMGPP (IN REF. 2).
FT	CONFLICT	532	532	T -> K (IN REF. 2).
FT	CONFLICT	682	682	Q -> K (IN REF. 2).
FT	CONFLICT	730	730	E -> D (IN REF. 2).
FT	CONFLICT	750	750	L -> R (IN REF. 2).
FT	CONFLICT	834	834	A -> T (IN REF. 2).
FT	CONFLICT	1035	1035	G -> A (IN REF. 2).
FT	CONFLICT	1068	1068	M -> L (IN REF. 2).
FT	CONFLICT	1285	1285	P -> R (IN REF. 2).
FT	CONFLICT	1400	1400	G -> A (IN REF. 2).
FT	CONFLICT	1611	1611	T -> S (IN REF. 2).
FT	CONFLICT	1729	1729	G -> A (IN REF. 2).
SQ	SEQUENCE	2142 AA; 227840 MW; 32DDF16B9B52420A CRC64;		
Query Match 5.0%; Score 110; DB 1; Length 2142;				
Best Local Similarity 24.1%; Pred No. 14;				
Matches 55; Conservative 29; Mismatches 94; Indels 50; Gaps 11;				
QY	178	LPSPDQSPGNATTSVTRDNYHLLTEEEFGVWSQSMKWHSQKSGSVFVRGPTQEPCC--	235	
DB	516	LPAPPAPPASAPTPETE-----PEEP-----AQAPPAQSTPTPGVAAAPTIV	558	
QY	236	-----SESQLKESF-VPPPTPKENKQEREDENWRLPPPPVAETVPSPSVTEIETPLQR	290	
DB	559	SGGSTSTSSGSGFEASPVPEQLPSKEG-----PEPPEEVPPTTTPPVKVEPKGDG	610	
QY	291	IPRTATIAGEPLGHCFTF--TISPAFVHSLNKKRQLELLREVEWPGRGHMAATCCKLQ	348	
DB	611	IGPTROPSPQGLGYPKYQKSLPRF-----QRQQEQQLLKQOQHOHQOQSGSAPPTP	664	
QY	349	V-EGQDRTMSLAAPVREAPPPP-----TCASSEPSVPALP--GADPQ	388	
DB	665	VPPSPPPQVTLGAVPAPQAPPPPPKALYFALGRP--PPMPNMFDP	710	

Search completed: December 25, 2002, 01:11:24  
Job time : 32 secs